

SEQUENCE LISTING

<110> Susan M. Freier

Mark P. Roach

<120> ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION

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gcc atg gat cgg atg aag aag atc aaa cgg cag ctg tca atg aca ctc 168

Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met Thr Leu

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cga ggt ggc cga ggc ata gac aag acc aat ggt gcc cct gag cag ata 216

Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln Ile

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ggc ctg gat gag agt ggt ggt ggc ggc agt gac cct gga gag gcc 264

Gly Leu Asp Glu Ser Gly Gly Gly Ser Asp Pro Gly Glu Ala

35 40 45

ccc aca cgt gct cct ggg gaa ctt cgt tct gca cgg ggc cca ctc 312

Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro Leu

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agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg tct gat 360

Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser Asp

65 70 75

ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg cag tct 408

Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln Ser
80 85 90 95

cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc tcc act 456
Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser Thr
100 105 110

gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg ctg cct 504
Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu Pro
115 120 125

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Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp Lys
130 135 140

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Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly Phe
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ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag ggt acc 648
Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly Thr
160 165 170 175

tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac ctt gtg 696
Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu Val
180 185 190

gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc tgc acc 744
Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr
195 200 205

gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc aac atc 792
Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala Asn Ile
210 215 220

gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc ctt gtc 840
Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr Leu Val
225 230 235

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Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp Cys Gly
240 245 250 255

aac atc atc aac atg cac aac gtg aaa ctg ttc ctg ttc cag ctg ctc 936
Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu Leu
260 265 270

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Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp Leu
275 280 285

aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag ctg gct 1032
Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
290 295 300

gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca tac tcc 1080
Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr Tyr Ser
305 310 315

aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg ctt ggg 1128
Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu Leu Gly
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Ser Thr Asp Tyr Ser Thr Gln Ile Asp Met Trp Gly Val Gly Cys Ile
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Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr Val
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Glu Glu Gln Leu His Phe Ile Phe Arg Ile Leu Gly Thr Pro Thr Glu
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Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro Arg Leu
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Asp Ser Asp Gly Ala Asp Leu Leu Thr Lys Leu Leu Gln Phe Glu Gly
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Arg Asn Arg Ile Ser Ala Glu Asp Ala Met Lys His Pro Phe Phe Leu
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agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc ata ttt 1512
Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser Ile Phe
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Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg Ser Ser
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Ser Met Pro Asp Ser Gly Arg Pro Ala Phe Arg Val Val Asp Thr Glu
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Phe

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